

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 26, 2004, 16:59:06 ; Search time 12,1928 seconds
(without alignments)
1996.498 Million cell updates/sec

Title: US-10-655-873-8
Perfect score: 1304
Sequence: 1 MWPPGASQPPSPAAATGL.....HAFRIRAVTIDRVMSYLNAS 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1304	100.0	interleukin 12A pr
2	844	49.4	interleukin 12 p35
3	98.5	7.6	hypothetical prote
4	97	7.4	DNA-directed RNA p
5	93.5	7.2	hypothetical prote
6	91	7.0	hypothetical prote
7	91	7.0	kinesin-related pr
8	90.5	6.9	protein kinase dra
9	90	6.9	hypothetical prote
10	89.5	6.9	hypothetical prote
11	89.5	6.9	hypothetical prote
12	89	6.8	pectinesterase (BC
13	88.5	6.8	hypothetical prote
14	87	6.7	hypothetical prote
15	86	6.6	hypothetical prote
16	86	6.6	glycoprotein B pre
17	86	6.6	probable glycoprot
18	86	6.6	glycoprotein B (im
19	85.5	6.6	hypothetical prote
20	85.5	6.6	probable valyl trn
21	85.5	6.6	hypothetical prote
22	85	6.5	hypothetical prote
23	85	6.5	hypothetical prote
24	84	6.4	trithorax homolog
25	83.5	6.4	estrogen-responsiv
26	83.5	6.4	hypothetical prote
27	83	6.4	hypothetical prote
28	83	6.4	glycoprotein B pre
29	83	6.4	probable membrane

30	82.5	6.3	460	2	B48057	farnesyl-diphospha
31	82.5	6.3	460	2	T40581	farnesyl-diphospha
32	82.5	6.3	583	2	S01496	lamin B - African
33	82.5	6.3	817	2	S53921	hypothetical prote
34	82	6.3	508	1	KRSHL2	keratin type II, m
35	82	6.3	542	2	T19925	hypothetical prote
36	82	6.3	554	2	T51213	hypothetical prote
37	82	6.3	808	2	A96791	hypothetical prote
38	82	6.3	958	2	T26621	hypothetical prote
39	82	6.3	1094	2	S22573	DNA-directed DNA p
40	81.5	6.2	542	2	A82965	hypothetical prote
41	81.5	6.2	561	2	T07649	hypothetical prote
42	81.5	6.2	603	2	T16655	hypothetical prote
43	81.5	6.2	873	2	H85134	polyubiquitin-like
44	81.5	6.2	3092	2	S46009	GTPase-activating
45	81	6.2	576	2	T48573	hypothetical prote

ALIGNMENTS

RESULT 1
B38957
interleukin 12A precursor [validated] - human
N:Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer cell
C:Species: Homo sapiens (man)
C:Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: B38957; A39359; A36055
R:Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.;
i, G.; Perussia, B.
J, Immunol. 146, 3074-3081, 1991
A:Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cy
A:Reference number: A38957; MUID:91201875; PMID:1673147
A:Accession: B38957
A:Molecule type: mRNA
A:Residues: 1-253 <WOL>
A:Cross-references: UNIPROT:O60595; GB:M65290
A:Note: it is uncertain whether Met-1 or Met-35 is the initiator
R:Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nabay
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A:Title: Coexpression of two distinct genes is required to generate secreted bioactive
A:Reference number: A39359; MUID:91239523; PMID:1674604
A:Accession: A39359
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 35-246, 'T', 248-253 <GUB>
A:Cross-references: GB:M65271; GB:M38443; NID:G180623; PIDN:AAA35694.1; PID:G180624
R:Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.;
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A:Title: Purification to homogeneity and partial characterization of cytotoxic lymphocy
A:Reference number: A36055; MUID:90370873; PMID:2204066
A:Accession: A36055
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 58-70, 'X', 72-82 <STE>
C:Genetics:
A:Gene: GDB:IL12A; NKSF1
A:Cross-references: GDB:127869; OMIM:161560
A:Map position: 3p12-3q13.2
C:Keywords: cytokine; glycoprotein; heterodimer
F:57-253/Product: interleukin 12A #status predicted <MAT>
F:127,141,251/Binding site: carbohydrate (Asn) #status predicted

Query Match				100.0%;	Score 1304;	DB 2;	Length 253;
Best Local Similarity				100.0%;	Pred. No. 3.5e-101;		
Matches 253;				Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MWPPGASQPPSPAAATGLHPAARPVSLQCRLSMCPARSLVATLVLLDHLSLARNLP	60				
Db	1	MWPPGASQPPSPAAATGLHPAARPVSLQCRLSMCPARSLVATLVLLDHLSLARNLP	60				
QY	61	VATDPGPFCLHSHQNLRAVSNMLQARQTLFPYPTCSSEIDHDTKDTSTVEACL	120				

Db 61 VATPDGMPFCLHSHSONLLRAVSNMLQKARQTLFYPCTSEBIDHEDITKDKTSTVEACL 120
QY 121 PLELTKNESCINRSFTINGSCILASRTSPFAMALCLSIYEDLKMYQVEFKTNMAKLL 180
Db 121 PLELTKNESCINRSFTINGSCILASRTSPFAMALCLSIYEDLKMYQVEFKTNMAKLL 180
QY 181 MPKQGFIDQNLAVIDELMQALNFSNTPVQKSSLEBPDFFYTKIKLCILLHAFRIRA 240
Db 181 MPKQGFIDQNLAVIDELMQALNFSNTPVQKSSLEBPDFFYTKIKLCILLHAFRIRA 240
QY 241 VTIDRVMSYLNAS 253
Db 241 VTIDRVMSYLNAS 253

RESULT 2
I56135
interleukin 12 p35 subunit - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56135
R:Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.; J. Immunol. 148, 3433-3440, 1992
A:Title: Cloning and Expression of Murine IL-12.
A:Reference number: I56135; MUID:92268481; PMID:1350290
A:Accession: I56135
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-215 <RES>
A:CROSS-references: UNIPROT:P43431; GB:M86672; NID:g198336; PID:g198337

Query Match 49.4%; Score 644; DB 2; Length 215;
Best Local Similarity 58.9%; Pred. No. 2.5e-46;
Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;

QY 35 MCPARSLLVATLVLDHLSLARNLPVATPDGMPFCLHSHSONLLRAVSNMLQKARQTL 94
Db 1 MCQSRYLLFLATLNLHLSLARVIPVSGP---ARCLSQSRNLLKTTDDMVKTAREKIK 56
QY 95 FYPCTSEEDHEDITKDKTSTVEACLPLELTKNESCINRSFTINGSCILASRTSPFM 154
Db 57 HYSCTAEDIDHEDITKDKTSTVEACLPLELTKNESCINRSFTINGSCILASRTSPFM 116
QY 155 ALCLSIYEDLKMYQVEFKTNMAKLLMDPKRQIFLDQNLAVIDELMQALNFSNTPVQK 214
Db 117 TLCLGSIYEDLKMYQVEFOAINAALQNNHQQIILDKGMLVAIDELMQSLNHNGETLRQK 176
QY 215 SSLEBPDFFYTKIKLCILLHAFRIRAVTIDRVMSYLNAS 253
Db 177 PPVGEADPYRVKMKLCILLHAFSTRVVTINRVNGYLSSA 215

RESULT 3
T45785
hypothetical protein F26013.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45785
R:Deiseny, M.; Berger, C.; Cooke, R.; Grellert, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23013
A:Accession: T45785
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438
A:CROSS-references: UNIPROT:Q9SC25; EMBL:AL13452
A:Experimental source: cultivar Columbia; BAC clone F26013
C:Genetics:
A:Map position: 3
A:Introns: 35/1; 67/2; 104/3; 326/3
A>Note: F26013.180

Query Match 7.6%; Score 98.5; DB 2; Length 438;

Best Local Similarity 25.6%; Pred. No. 1.5;
Matches 42; Conservative 27; Mismatches 48; Indels 47; Gaps 9;

QY 3 PPGSASQPPSPAAATGLHAPARPVSLQCLSMC---PARSLLVATLVLDHLSLARN 58
Db 272 PKGRSASGLPFTFGSTHTTTTPKSIKPSATVADSTPRGKLSRASVQMAINHLDLARN 331
QY 59 LPVAT---PDQMFPCLLHSHSONLLRAVSNMLQKARQTLFYPCTSEBIDHEDITKDKT 105
Db 332 GKVSHTFTSSPMLYF---HS---IRSSSSGLRK-----PCGSSEGCSSSNHEEDBG 377
QY 106 EDITKDKTSTVEACLPLELTKNESC-----LN---SRETSPITN 141
Db 378 RSLTKEGNTE-----NKNDARYDALLNVKVKOTNWLIN 413

RESULT 4
T07321
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Chlorella vulgaris chloroplast
C:Species: Chlorella vulgaris
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07321
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Teudzuki, J.; Naka
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl
A:Reference number: Z15985; MUID:97303241; PMID:9159184
A:Accession: T07321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1301 <WAK>
A:CROSS-references: UNIPROT:P56299; EMBL:AB001684; NID:g2224352; PIDN:BAA57969.1; PID:g
C:Genetics:
A:Gene: rpoB
A:Genome: chloroplast
C:Superfamily: DNA-directed RNA polymerase beta chain
C:Keywords: chloroplast; nucleotidyltransferase

Query Match 7.4%; Score 97; DB 2; Length 1301;
Best Local Similarity 22.4%; Pred. No. 7.8;
Matches 54; Conservative 33; Mismatches 92; Indels 62; Gaps 10;

QY 44 VATLVLDHLSLARNLPVATPDGMPFCLHSHSONLLRAVSNMLQKARQTL 94
Db 574 VATRITTSQVGLQNISVAT---SLIPFLEHNDANRALMGSNMQROAVPLLPQAPLVGT 630
QY 95 -FYPCTSEIDEH-----DITKDKTSTVEACL-----LELTKNESC 130
Db 631 GLESRVIGDVNHSQASKTGFTTKVSTSKIQVLSPRKTKAQVSVFHSVLFSLNKKKKSL 690
QY 131 LNSRETSPITNGSCL-----ASRKTSPFMALCLSIYEDLKMYQVEFKTNMAKLLMDP 183
Db 691 LNSEKQSFSGKIGFTTKLQKSNLKNIFPSA--QKALYQENSSPDLPKFAQNR--LFIP 746
QY 184 KRQIFLDQNLAVIDELMQALNFSNTPVQKSSLEBPDFFYTKIKLCILLHAFRIRA 228
Db 747 KMTFSLAQNFSRKIPFLSFLLKKKKPRPNPKKFFRSSDSFVNMKHKHLHSEDFRNKVE 806
QY 229 L 229
Db 807 I 807

RESULT 5
G83771
hypothetical protein BH0975 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83771
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB8650; MUID:20512582; PMID:11059132
A:Accession: G83771

KW Human; interleukin 12; IL-12; heterodimeric complex; immunogenic;
 KW Leishmania; antigen; leishmaniasis; cell-mediated immunity; adjuvant;
 KW TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer;
 KW vaccine; cell surface; membrane; glycoprotein; antigen presenting cell.
 XX
 OS Homo sapiens.

XX US5571515-A.
 XX 05-NOV-1996.

XX 17-JUN-1994; 94US-00265087.
 XX 18-APR-1994; 94US-00229282.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Trinchieri G, Scott P;
 XX WPI; 1996-505347/50.
 XX N-PSDB; AAT48098.

XX Immunogenic compsn. to improve cell mediated immune response - contains
 XX soluble leishmania antigen and interleukin-12 as adjuvant.
 XX Disclosure; Col 17-22; 22pp; English.

XX This is the amino acid sequence of the human interleukin (IL)-12 40 kD
 XX subunit. IL-12 is a heterodimeric complex composed of the 40 kD subunit
 XX and a 30 kD subunit (AAW07399). The complex is used in a novel
 XX immunogenic composition comprising a soluble Leishmania antigen with IL-
 XX 12, for protection against leishmaniasis. The addition of IL-12 improves
 XX cell-mediated immunity by inducing TH1 helper cells (as opposed to TH2
 XX cells which are induced by alum adjuvant) and does not cause uncontrolled
 XX release of other cytokines (in contrast to bacterial adjuvants). IL-12
 XX can also be used as a cancer vaccine by association with the protein B7,
 XX a soluble, cell-surface (membrane)-bound glycoprotein which is expressed
 XX in antigen presenting cells. (Updated on 25-MAR-2003 to correct PF
 XX field.)

XX SQ Sequence 328 AA;

Query Match 100.0%; Score 1758; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.5e-148;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCHQQLVISWFSVFLASPLVAIWELKKDVVVELDWPDPAGEMVLTCDTPBEDGITW 60
 DB 1 MCHQQLVISWFSVFLASPLVAIWELKKDVVVELDWPDPAGEMVLTCDTPBEDGITW 60
 QY 61 TLDQSSVLGSGKTLTIQVKEFGDAGQYTCBKGEVLSHLSLLHKKEDGIWSTDILKQD 120
 DB 61 TLDQSSVLGSGKTLTIQVKEFGDAGQYTCBKGEVLSHLSLLHKKEDGIWSTDILKQD 120
 QY 121 KEPKNKTFLRCEAKNYSGRFTCWLTITISDLTFSVKSRRGSDPQGVTCGAATLSARV 180
 DB 121 KEPKNKTFLRCEAKNYSGRFTCWLTITISDLTFSVKSRRGSDPQGVTCGAATLSARV 180
 QY 181 RGNKKEYSVCEQDSACPAERSLPIEVNMDVAVHKLKYNYSSTPIRDIIPDPKPN 240
 DB 181 RGNKKEYSVCEQDSACPAERSLPIEVNMDVAVHKLKYNYSSTPIRDIIPDPKPN 240
 QY 241 LQKPLKNSRQVSWYEPDWTSTPHSYFSLTFCVQVQGSKRKDKRVFTDKTSATVIC 300
 DB 241 LQKPLKNSRQVSWYEPDWTSTPHSYFSLTFCVQVQGSKRKDKRVFTDKTSATVIC 300
 QY 301 RKNASISVRAQDRYYSNSENWASVPSCS 328
 DB 301 RKNASISVRAQDRYYSNSENWASVPSCS 328

RESULT 4

AAW24235

ID AAW24235 standard; protein; 328 AA.

XX AC AAW24235;

XX DT 25-MAR-2003 (revised)
 XX DT 18-MAR-1998 (first entry)

XX DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor.
 KW Cytotoxic lymphocyte maturation factor; CLMP; 40 kDa subunit;
 KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
 KW CLMP bioactivity inhibition; affinity ligand; transplacental;
 KW cytotoxic T cell proliferation.

XX OS Homo sapiens.

XX FN EP790255-A2.
 XX PD 20-AUG-1997.

XX PF 09-DEC-1990; 97EP-00104656.
 XX PR 22-DEC-1989; 89US-00455708.
 XX PR 09-MAY-1990; 90US-00520935.
 XX PR 27-AUG-1990; 90US-00572284.
 XX PR 09-DEC-1990; 90EP-00123670.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
 XX Podlanski EJ, Stern AS;

XX WPI; 1997-404698/38.
 XX N-PSDB; AAT77849.

XX Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
 XX affinity ligands, assay reagents and medicaments.
 XX Claim 2; Fig 25; 80pp; English.
 CC The present sequence represents the 40 kDa subunit of cytotoxic
 CC lymphocyte maturation factor (CLMP) protein. The natural CLMP protein is
 CC a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa
 CC subunit) are bonded together via one or more disulphide bonds. CLMP
 CC protein is produced by a human B lymphoblastoid cell line. CLMP
 CC synergistically induces, in the presence of interleukin-2, the cytolytic
 CC activity of lymphokine activated killer cells. CLMP is also capable of
 CC stimulating T-cell growth. A novel antibody directed against an epitope
 CC of CLMP protein (see AAW24237 for epitope) is capable of neutralising
 CC and/or inhibiting CLMP bioactivity. This antibody may be used as an
 CC affinity ligand for purifying the CLMP protein. The antibody can also be
 CC used as an assay reagent for detecting the CLMP protein, and as a
 CC medicament for selectively blocking the proliferation and activation of
 CC cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
 CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 328 AA;

Query Match 100.0%; Score 1758; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.5e-148;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCHQQLVISWFSVFLASPLVAIWELKKDVVVELDWPDPAGEMVLTCDTPBEDGITW 60
 DB 1 MCHQQLVISWFSVFLASPLVAIWELKKDVVVELDWPDPAGEMVLTCDTPBEDGITW 60
 QY 61 TLDQSSVLGSGKTLTIQVKEFGDAGQYTCBKGEVLSHLSLLHKKEDGIWSTDILKQD 120
 DB 61 TLDQSSVLGSGKTLTIQVKEFGDAGQYTCBKGEVLSHLSLLHKKEDGIWSTDILKQD 120
 QY 121 KEPKNKTFLRCEAKNYSGRFTCWLTITISDLTFSVKSRRGSDPQGVTCGAATLSARV 180

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OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 09:32:55 ; Search time 437.322 Seconds
(without alignments)
15189.855 Million cell updates/sec

Title: US-10-655-873-11
Perfect score: 1193
Sequence: 1 tgaagatcagctattagaag.....taaaagtgtaagttcacaact 1193

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues
Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1193	100.0	1193	15	US-10-284-740-13
2	1193	100.0	1193	16	US-10-641-643-1302
3	1193	100.0	1193	17	US-10-283-975A-258
4	1193	100.0	1193	17	US-10-654-796-6
5	1193	100.0	1193	17	US-10-654-763-6
6	1193	100.0	1193	18	US-10-733-878-280
7	963.2	80.7	987	10	US-09-882-945A-141
8	963.2	80.7	987	18	US-10-807-114-141
9	718.8	60.3	5961	15	US-10-429-802-35
10	718.8	60.3	5961	16	US-10-430-503-26
11	501.8	42.1	601	15	US-10-267-384-168
12	499.4	41.9	501	16	US-10-411-037-19
13	499.4	41.9	501	16	US-10-411-026-19
14	499.4	41.9	501	16	US-10-410-962-19
15	499.4	41.9	501	16	US-10-411-045-19
16	499.4	41.9	501	17	US-10-410-930-19
17	499.4	41.9	501	17	US-10-410-997-19
18	499.4	41.9	501	17	US-10-411-012-19
19	499.4	41.9	501	17	US-10-287-994-19
20	499.4	41.9	501	17	US-10-410-913-19
21	499.4	41.9	501	18	US-10-276-642-1
22	496.4	41.6	498	17	US-10-432-777-13
23	433.2	36.3	438	15	US-10-151-469-22
24	433.2	36.3	438	16	US-10-422-523-17
25	347	29.1	567	15	US-10-151-469-21
26	347	29.1	567	16	US-10-422-523-16
27	347	29.1	583	15	US-10-205-534-9
28	347	29.1	623	15	US-10-205-534-7
29	325.2	27.3	538	15	US-10-151-469-20
30	325.2	27.3	538	16	US-10-422-523-15
31	306	25.6	498	13	US-10-116-273-42
32	306	25.6	498	15	US-10-195-707B-42
33	306	25.6	498	15	US-10-186-962-5
34	282.2	23.7	375	15	US-10-369-495-3
35	245.6	20.6	368	16	US-10-131-827-8202
36	222.6	18.7	322	16	US-10-131-827-8477
37	213	17.9	514	16	US-10-131-827-8745
38	191.6	16.1	576	16	US-10-131-827-8181
39	185.2	15.5	594	16	US-10-131-827-8744
40	185	15.5	185	9	US-09-864-761-19121
41	181.6	15.2	480	9	US-09-864-761-2388
42	172.2	14.4	308	15	US-10-279-061-71
43	172.2	14.4	309	15	US-10-279-061-81
44	172.2	14.4	393	15	US-10-279-061-87
45	169.8	14.2	370	16	US-10-131-827-8700

ALIGNMENTS

RESULT 1
US-10-284-740-13
; Sequence 13, Application US/10284740
; Publication NO. US20030138404A1
; GENERAL INFORMATION:
; APPLICANT: Maroun, Leonard E.
; TITLE OF INVENTION: INTERFERON ANTAGONISTS USEFUL FOR THE TREATMENT OF INTERFERON RE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 18448/2002
; CURRENT APPLICATION NUMBER: US/10/284,740
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/845,260
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/067,398
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 08/502,519
; PRIOR FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(609)
; OTHER INFORMATION:
US-10-284-740-13

Query Match 100.0%; Score 1193; DB 15; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-244;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGATCAGCTATTAGAAGAGATCAGTTAGTCTTTGGACCTGTGATCAGCTTGAT 60
|||||

Db 1 TGAAGATCAGCTATTAGAGAGAGAAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGAT 60
Qy 61 ACAAGAACTACTGATTTTCAAACTTTCTTTGGCTTAAATTTCTCGGAAACGATGAATATATACA 120
Db 61 ACAAGAACTACTGATTTTCAAACTTTCTTTGGCTTAAATTTCTCGGAAACGATGAATATATACA 120
Qy 121 AGTTATATCTTGGCTTTTTCAGCTCTGCATCGTTTTTGGGTTCTCTTGGCTGTGTACTGCGAG 180
Db 121 AGTTATATCTTGGCTTTTTCAGCTCTGCATCGTTTTTGGGTTCTCTTGGCTGTGTACTGCGAG 180
Qy 181 GACCCATATGTAAGAGAGAGCAAACTTAAAGATATTTTAAATGATGAGGTCATTCAGAT 240
Db 181 GACCCATATGTAAGAGAGAGCAAACTTAAAGATATTTTAAATGATGAGGTCATTCAGAT 240
Qy 241 GTAGCGGATATGGAACCTTTTCTTAGGCATTTTGAAGATTTGAAAGAGAGAGAGTGCAC 300
Db 241 GTAGCGGATATGGAACCTTTTCTTAGGCATTTTGAAGATTTGAAAGAGAGAGAGTGCAC 300
Qy 301 AGAAAAATATGAGAGAGCAAAATTTCTCTTTTACTTCAAACTTTTAAAAACTTTTAAA 360
Db 301 AGAAAAATATGAGAGAGCAAAATTTCTCTTTTACTTCAAACTTTTAAAAACTTTTAAA 360
Qy 361 GATGACAGAGCATCCAAAGAGTGTGGAGACCATCAAGGAGAGACATCAATGTCAGGTTT 420
Db 361 GATGACAGAGCATCCAAAGAGTGTGGAGACCATCAAGGAGAGACATCAATGTCAGGTTT 420
Qy 421 TTCAATAGCAACAAAGAGAGAGATGATGATCTTGAAGAGCTGACTAAATTTATTCGGTAACT 480
Db 421 TTCAATAGCAACAAAGAGAGAGATGATGATCTTGAAGAGCTGACTAAATTTATTCGGTAACT 480
Qy 481 GACTTGAAATGTCACAGCAAGCAATATCATGAATCATCTCAAGTGATGCGTGAATGTCG 540
Db 481 GACTTGAAATGTCACAGCAAGCAATATCATGAATCATCTCAAGTGATGCGTGAATGTCG 540
Qy 541 CCAGCAGCTAAACAGGAGAGGAGAGAGAGTGCAGTCTGTTTCAAGGTCGAAGACCA 600
Db 541 CCAGCAGCTAAACAGGAGAGGAGAGAGAGTGCAGTCTGTTTCAAGGTCGAAGACCA 600
Qy 601 TCCAGATTAATGTTGTCCTGCTGCAATATTTGAATTTTAAATCTAAATCTATTATTATTA 660
Db 601 TCCAGATTAATGTTGTCCTGCTGCAATATTTGAATTTTAAATCTAAATCTATTATTATTA 660
Qy 661 TATTAAACATTTATATATGAGGATATATTTTATAGACTCATCAATCAATCAATCAATTTA 720
Db 661 TATTAAACATTTATATATGAGGATATATTTTATAGACTCATCAATCAATCAATCAATTTA 720
Qy 721 TAATAGCAACTTTTGTGTAATGAATGAATGAATCATCTATTAATATATATATATATTAAT 780
Db 721 TAATAGCAACTTTTGTGTAATGAATGAATGAATCATCTATTAATATATATATATATTAAT 780
Qy 781 CCTATATCTGTGATGCTCTCACTTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 CCTATATCTGTGATGCTCTCACTTAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 841 GTGATTAACAGGCTTTATCTCAGGGGCCAACTAGGAGCCCAACCTTAAGCAAGATCCCATG 900
Db 841 GTGATTAACAGGCTTTATCTCAGGGGCCAACTAGGAGCCCAACCTTAAGCAAGATCCCATG 900
Qy 901 GGTGTGTGTTTATTTCACTTGATGATCAATGAACACTTATATAGTGAAGTACTATTC 960
Db 901 GGTGTGTGTTTATTTCACTTGATGATCAATGAACACTTATATAGTGAAGTACTATTC 960
Qy 961 CAGTTACTGCGGTTTGAATAATGCTGCAATCTGAGCAGTGTCTTAAATGGCATGTCA 1020
Db 961 CAGTTACTGCGGTTTGAATAATGCTGCAATCTGAGCCAGTGTCTTAAATGGCATGTCA 1020
Qy 1021 GACAGAACTTGAATGTGTGAGTGAACCTGATGAGAAACATAGCATCTCAGGAGATTTTCAT 1080
Db 1021 GACAGAACTTGAATGTGTGAGTGAACCTGATGAGAAACATAGCATCTCAGGAGATTTTCAT 1080
Qy 1081 GCCTGTGCTTCCAAATATTTGTCAGAACTGTGACTGTACCCAAATGGAAGTAACTCAT 1140
Db 1081 GCCTGTGCTTCCAAATATTTGTCAGAACTGTGACTGTACCCAAATGGAAGTAACTCAT 1140

Qy 1141 TTGTTAAATTTATCAATATCTAATATATATATATATATATATATATATATATATATATAT 1193
Db 1141 TTGTTAAATTTATCAATATCTAATATATATATATATATATATATATATATATATATAT 1193

RESULT 2

US-10-641-643-1302
; Sequence 1302, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g32691
; SEQUENCE DESCRIPTION: SEQ ID NO: 1302 :
US-10-641-643-1302

Query Match 100.0%; Score 1193; DB 16; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2,6e-244;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGATCAGCTATTAGAGAGAGAAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGAT 60
Db 1 TGAAGATCAGCTATTAGAGAGAGAAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGAT 60
Qy 61 ACAGAACTACTGATTTTCAAACTTTCTTTGGCTTAAATTTCTCTCGGAAACGATGAATATACA 120
Db 61 ACAGAACTACTGATTTTCAAACTTTCTTTGGCTTAAATTTCTCTCGGAAACGATGAATATACA 120
Qy 121 AGTTATATCTTGGCTTTTTCAGCTCTGCATCGTTTTTGGGTTCTCTTGGCTGTGTACTGCGAG 180
Db 121 AGTTATATCTTGGCTTTTTCAGCTCTGCATCGTTTTTGGGTTCTCTTGGCTGTGTACTGCGAG 180
Qy 181 GACCCATATGTAAGAGAGAGCAAACTTAAAGATATTTTAAATGATGAGGTCATTCAGAT 240
Db 181 GACCCATATGTAAGAGAGAGCAAACTTAAAGATATTTTAAATGATGAGGTCATTCAGAT 240

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 26, 2004, 10:00:30 ; Search time 31.5556 Seconds
(without alignments)
1887.118 Million cell updates/sec

Title: US-10-655-873-12

Perfect score: 856

Sequence: 1 MKYTSYLAFOLCIVLGLSLG.....AKTGKRSQMLFQGRASQ 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	856	100.0	166	1	AAP93414 IFN211
2	856	100.0	166	7	ADP76401
3	856	100.0	166	7	ADM13723
4	856	100.0	166	8	ADP12492
5	856	100.0	166	8	ADP19766
6	856	100.0	166	8	ADQ09094
7	852	99.5	166	1	AAP30093
8	852	99.5	166	1	AAP40122
9	852	99.5	166	1	AAP40153
10	852	99.5	166	1	AAP40157
11	852	99.5	166	1	AAP50233
12	852	99.5	166	2	AAW70582
13	852	99.5	166	4	ABW99130
14	852	99.5	166	5	ABE15823
15	852	99.5	166	5	AAU78100
16	852	99.5	166	5	AAU98670
17	852	99.5	166	5	ABW07440
18	852	99.5	166	6	ABR55948
19	852	99.5	166	6	ABR40017
20	852	99.5	166	6	ABP56461
21	852	99.5	166	6	ADA94887
22	852	99.5	166	7	ADC78909
23	852	99.5	166	8	ADG45031
24	852	99.5	166	8	ADJ56129
25	852	99.5	166	8	ADJ25952

ALIGNMENTS

RESULT 1

AAP93414
ID AAP93414 standard; protein; 166 AA.

XX AC AAP93414;

XX DT 27-APR-1990 (first entry)

XX DE IFN211 , IFN-gamma mutant.

XX KW Interferon-gamma; mutant; IFN211.

XX OS Homo sapiens.

XX PN BP343388-A.

XX PD 29-NOV-1989.

XX PF 25-APR-1989; 89EP-00107460.

XX PR 25-APR-1988; 88US-00185219.

XX PA (PHIP) PHILLIPS PETROLEUM CO.

XX PI Thill GP, Davis GR;

XX DR WPI; 1989-349507/48.

XX N-PSDB; AAN92425.

XX PT Enhanced prodn. of interferon-gamma - using methylotrophic yeast, esp. Pichia pastoris, transformed with linear integrative site-specific vector.

XX PS Disclosure; Page 7; 26pp; English.

XX CC IFN211 is a mutated form of IFN-gamma structural gene created by deleting the signal sequence by creating an EcoRI site and second start codon at approx. 66, 67, and 68 of the wt sequence. The mutant gene is used to construct IFN-gamma cytoplasmic expression vectors esp. methylotrophic yeast vectors for transfection of Pichia pastoris. See also AAP93416

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 856; DB 1; Length 166;

Best Local Similarity 100.0%; Pred. No. 2e-77;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKYTSYLAFOLCIVLGLSLGVCQDPYVKEAENLKKYFNAGHSVDVADNGTLFLGLIKWK 60

Db 1 MKTTSYLAFQLCIVLGLSLGVCYQDPYVKEAENLKVFYFNAGHSDVADNGTLFLGLKNWK 60
 Qy 61 EESDRKIMQSIQVSYFYFKLFFKFKDDQSIQKSVETIKEDNMNVFFNSNKKRRDDFEKLTN 120
 Db 61 EESDRKIMQSIQVSYFYFKLFFKFKDDQSIQKSVETIKEDNMNVFFNSNKKRRDDFEKLTN 120
 Qy 121 YSVTDNLNVORKAIEHLIQVMAELSPAATGKRKRQSMQLFQGRASQ 166
 Db 121 YSVTDNLNVORKAIEHLIQVMAELSPAATGKRKRQSMQLFQGRASQ 166

RESULT 2
 ID ADF76401 standard; protein; 166 AA.
 XX ADF76401;
 XX 26-FEB-2004 (first entry)
 XX Novel human secreted and transmembrane protein SeqID 74.
 XX human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX Homo sapiens.
 OS
 XX WO2003072035-A2.
 PN
 XX 04-SEP-2003.
 PD
 XX 21-FEB-2003; 2003WO-US005241.
 PF
 XX 22-FEB-2002; 2002US-0359461P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WL, Wu TD;
 PI
 XX WPI; 2003-721702/68.
 DR N-PSDB; ADF76400.
 XX
 XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.
 XX
 XX Claim 10; SEQ ID NO 74; 918pp; English.
 PS
 XX This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neuropeptides or hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequence of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the

CC invention.
 XX SQ Sequence 166 AA;
 Query Match 100.0%; Score 856; DB 7; Length 166;
 Best Local Similarity 100.0%; Pred. No. 28-77; Indels 0; Gaps 0;
 Matches 166; Conservative 0; Mismatches 0;
 Qy 1 MKTTSYLAFQLCIVLGLSLGVCYQDPYVKEAENLKVFYFNAGHSDVADNGTLFLGLKNWK 60
 Db 1 MKTTSYLAFQLCIVLGLSLGVCYQDPYVKEAENLKVFYFNAGHSDVADNGTLFLGLKNWK 60
 Qy 61 EESDRKIMQSIQVSYFYFKLFFKFKDDQSIQKSVETIKEDNMNVFFNSNKKRRDDFEKLTN 120
 Db 61 EESDRKIMQSIQVSYFYFKLFFKFKDDQSIQKSVETIKEDNMNVFFNSNKKRRDDFEKLTN 120
 Qy 121 YSVTDNLNVORKAIEHLIQVMAELSPAATGKRKRQSMQLFQGRASQ 166
 Db 121 YSVTDNLNVORKAIEHLIQVMAELSPAATGKRKRQSMQLFQGRASQ 166

RESULT 3
 ADM13723
 ID ADM13723 standard; protein; 166 AA.
 XX ADM13723;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human interferon-gamma protein.
 DE
 XX Interferon; IFN; Alzheimer's disease; Down syndrome; infant encephalitis;
 KW autoimmune disease; HIV; AIDS-associated dementia; lupus erythematosus;
 KW ulcerative colitis; Hashimoto's disease; amyotrophic lateral sclerosis;
 KW Goodpasture's syndrome; therapy; acquired immunodeficiency syndrome;
 XX AIDS; human.
 XX Homo sapiens.
 OS
 XX US2003138404-A1.
 PN
 XX 24-JUL-2003.
 PD
 XX 31-OCT-2002; 2002US-00284740.
 PF
 XX 14-JUL-1995; 95US-00502519.
 PR 28-APR-1998; 98US-00087398.
 PR 30-APR-2001; 2001US-00845260.
 XX (MEIO-) METOGEN BIOTECHNOLOGY CORP.
 PA
 XX Maroun LE;
 PI
 XX WPI; 2003-829690/77.
 DR N-PSDB; ADM13724.
 DR GENE BANK; X13274.
 XX
 XX Composition for preventing or decreasing pathological effects of disease
 PT that are associated with increased level of or heightened responsiveness
 PT to interferon, comprises at least two isolated interferon binding
 PT proteins.
 XX
 XX Disclosure; Fig 7B; 38pp; English.
 PS
 XX The present invention provides composition for preventing or decreasing
 CC pathological effects of a disease that are associated with an increased
 CC level of or a heightened responsiveness to interferon (IFN) where the
 CC composition inhibits the activity of one or more IFN. The invention is
 CC useful for treating diseases such as Alzheimer's disease, Down syndrome,
 CC infant encephalitis, autoimmune diseases such as lupus erythematosus,
 CC ulcerative colitis, Hashimoto's disease, amyotrophic lateral sclerosis
 CC and Goodpasture's syndrome and HIV where the administration of the
 CC antagonist prevents or ameliorates AIDS (acquired immunodeficiency